

Appl. Serial No. 10/727,516  
Response to Official Action of August 10, 2005

IN THE CLAIMS

Please amend the claims as follows:

Claims 1-43 (Cancelled)

Claim 44 (Currently Amended): An isolated coryneform bacterium, which has been modified to express a decreased amount of malate dehydrogenase or to express a malate dehydrogenase with decreased activity compared to the corresponding unmodified strain, wherein said malate dehydrogenase has at least [[90-]] 95% homology to SEQ ID NO: 3.

Claim 45 (Currently Amended): The isolated coryneform bacterium of Claim 44, wherein the [[gene]] polynucleotide encoding said malate dehydrogenase has been eliminated.

Claim 46 (Currently Amended): The isolated coryneform bacterium of Claim 44, wherein expression of the [[gene]] polynucleotide encoding said malate dehydrogenase has been ~~inactivated~~ attenuated.

Claim 47 (Currently Amended): The isolated coryneform bacterium of Claim 44, wherein the expression of the [[gene]] polynucleotide encoding said malate dehydrogenase has been attenuated by modification of at least one operator, promoter, attenuator, ribosome binding site, or start codon, which is operably associated with said [[*mdhA* gene]] polynucleotide.

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Claim 48: (Currently Amended) The isolated coryneform bacterium of Claim 44, which expresses said malate dehydrogenase with decreased activity compared to the corresponding unmodified strain.

Claim 49 (Previously Presented): The isolated coryneform bacterium of Claim 44, which is of the genus *Corynebacterium* or *Brevibacterium*.

Claim 50 (Previously Presented): The isolated coryneform bacterium of Claim 44, which is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, and *Brevibacterium divaricatum*.

Claim 51 (Previously Presented): The isolated coryneform bacterium of Claim 44 which comprises pEMmdhAint.

Claim 52 (Previously Presented): A process for making an L-amino acid comprising:

- a) culturing the bacterium of Claim 44 in a medium suitable for the production of said L-amino acid by fermentation, and
- b) recovering said L-amino acid from the culture medium or from the bacterial cells.

Claim 53 (Previously Presented): The process of Claim 52, wherein said amino acid is L-lysine.

Claim 54 (Previously Presented): The process of Claim 52, wherein said amino acid is L-glutamate.

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Claim 55 (Currently Amended): The process of Claim 52, wherein in said bacterium the expression of the ~~the~~ [[*mdhA* gene]] polynucleotide encoding said malate dehydrogenase has been eliminated or ~~inactivated~~ attenuated.

Claim 56 (Currently Amended): The process of Claim 52, wherein in said bacterium the expression of the ~~the~~ [[gene]] polynucleotide encoding said malate dehydrogenase has been attenuated by modification of at least one, operator, promoter, attenuator, ribosome binding site, or start codon, which is operably associated with said ~~the~~ [[*mdhA* gene]] polynucleotide encoding said malate dehydrogenase.

Claim 57 (Currently Amended): The process of Claim 52, wherein said bacterium which expresses said malate dehydrogenase with decreased activity compared to the corresponding unmodified strain.

Claim 58 (Previously Presented): The process of Claim 52, wherein said bacterium is at least one selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, and *Brevibacterium divaricatum*.

Claim 59 (Previously Presented): The process of Claim 52, wherein said bacterium is *Corynebacterium glutamicum*.

Claim 60 (Currently Amended): The process of Claim 52, wherein said bacterium further comprises at least one [[gene]] polynucleotide whose expression is enhanced compared to an unmodified starting strain selected from the group consisting of:

- the *dapA* [[gene]] polynucleotide which codes for dihydrodipicolinate synthase,
- the *eno* [[gene]] polynucleotide which codes for enolase,
- the *zwf* [[gene]] polynucleotide which codes for ~~the *zwf* gene product~~ glucose-6-phosphate dehydrogenase,
- the *pyc* [[gene]] polynucleotide which codes for pyruvate carboxylase, and
- the *lysE* [[gene]] polynucleotide which codes for lysine exporter.

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Claim 61 (Currently Amended): The process of Claim 52, wherein said bacterium further comprises at least one [[gene]] polynucleotide whose expression is attenuated (compared to an unmodified starting strain) selected from the group consisting of:

the *pck* gene polynucleotide which codes for phosphoenol pyruvate carboxykinase,  
the *pgi* gene polynucleotide which codes for glucose 6-phosphate isomerase, and  
the *poxB* gene polynucleotide which codes for pyruvate oxidase.

Claim 62 (Previously Presented): The process of Claim 52, which is a batch process.

Claim 63 (Previously Presented): The process of Claim 52, which is a fed batch or repeated fed batch process.

Claim 64 (Previously Presented): The process of Claim 52, which is a continuous process.

Claim 65 (Currently Amended) The process of Claim [[44]] 52, wherein said bacterium has been modified to express a decreased amount of malate dehydrogenase

Claim 66 (Currently Amended): The bacterium of claim 65, wherein said malate dehydrogenase has the N-terminal amino acid residues ~~shown in~~ of SEQ ID NO: 1.

Claim 67 (Previously Presented): The bacterium of claim 66, wherein said malate dehydrogenase comprises the amino acid sequence of SEQ ID NO: 3.

Claim 68 (Currently Amended): The bacterium of claim 67, wherein said malate dehydrogenase is encoded by a polynucleotide comprising ~~the~~ nucleotides sequence 536 to 1519 of SEQ ID NO: 2.

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Claim 69 (Previously Presented): The bacterium of claim 68, wherein said  
polynucleotide comprises SEQ ID NO: 2.